



#8

## SEQUENCE LISTING

&lt;110&gt; GLUCKSMANN, MARIA ALEXANDRA

<120> 93870, A HUMAN G-PROTEIN COUPLED  
RECEPTOR AND USES THEREFOR

&lt;130&gt; MPI2001-021P1RCP1M

&lt;140&gt; 10/085,233

&lt;141&gt; 2002-02-28

&lt;150&gt; 60/272,677

&lt;151&gt; 2001-03-01

&lt;160&gt; 6

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1684

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (147)...(1085)

<223> n at position 1384 can be any  
nucleotide

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tggaaaggat agactggata agagatgctc agctaaggga gttcctggat ggcctttaga 120  
ttgatacacc aatccctctga aattgc atg caa aaa tgt gac ttc cca agt atg 173  
Met Gln Lys Cys Asp Phe Pro Ser Met  
1 5

cct ggc cac aat acc tcc agg aat tcc tct tgc gat cct ata gtg aca 221  
Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr  
10 15 20 25

ccc cac tta atc agc ctc tac ttc ata gtg ctt att ggc ggg ctg gtg 269  
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val  
30 35 40

ggg gtc att tcc att ctt ttc ctc ctg gtg aaa atg aac acc cgg tca 317  
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser  
45 50 55

gtg acc acc atg gcg gtc att aac ttg gtg gtg gtc cac agc gtt ttt 365  
Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe  
60 65 70

ctg ctg aca gtg cca ttt cgc ttg acc tac ctc atc aag aag act tgg 413  
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp  
75 80 85

atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt gcc atg ctg cac atc 461  
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile  
90 95 100 105

cac atg tac ctc acg ttc cta ttc tat gtg gtg atc ctg gtc acc aga 509  
His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr Arg  
110 115 120

tac ctc atc ttc ttc aag tgc aaa gac aaa gtg gaa ttc tac aga aaa		557	
Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg Lys			
125	130	135	
ctg cat gct gtg gct gcc agt gct ggc atg tgg acg ctg gtg att gtc		605	
Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile Val			
140	145	150	
att gtg gta ccc ctg gtt gtc tcc cggtat gga atc cat gag gaa tac		653	
Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu Tyr			
155	160	165	
aat gag gag cac tgt ttt aaa ttt cac aaa gag ctt gct tac aca tat		701	
Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr Tyr			
170	175	180	185
gtg aaa atc atc aac tat atg ata gtc att ttt gtc ata gcc gtt gct		749	
Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val Ala			
190	195	200	
gtg att ctg ttg gtc ttc cag gtc ttc atc att atg ttg atg gtg cag		797	
Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val Gln			
205	210	215	
aag cta cgc cac tct tta cta tcc cac cag gag ttc tgg gct cag ctg		845	
Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln Leu			
220	225	230	
aaa aac cta ttt ttt ata ggg gtc atc ctt gtt tgt ttc ctt ccc tac		893	
Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro Tyr			
235	240	245	
cag ttc ttt agg atc tat tac ttg aat gtt gtg acg cat tcc aat gcc		941	
Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn Ala			
250	255	260	265
tgt agc agc aag gtt gca ttt tat aac gaa atc ttc ttg agt gta aca		989	
Cys Ser Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val Thr			
270	275	280	
gca att agc tgc tat gat ttg ctt ctc ttt gtc ttt ggg gga agc cat		1037	
Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser His			
285	290	295	
tgg ttt aag caa aag ata att ggc tta tgg aat tgt gtt ttg tgc cgt		1085	
Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys Arg			
300	305	310	
tagccacaaa ctacagtatt catatggct tcctttatat tgggataaaa atgggtatag	1145		
gggaggtaag aatggtattt cattacttga tcaaaaccat gccttgatgt accaaaaaca	1205		
aaaggactat aaaaatgcag agcccttattt gtgtccctta tggatccctt cccatctctg	1265		
agtatggcc gtacaaagac cagtgttgtt gaatccacct ggatgtgcatttattacatta	1325		
tttcccgta cagaatgtct gtgtggccca tgaaagcaac ataggtttta agagtttna	1385		
gagtttcatc agctcattct aagttccctt gtttgaagca tggctcttta ggtttggac	1445		
tgaactcaga ccttagttc ttttcatccc acttcaccat aggttaagtttattctggcca	1505		
ccacccagct ccaaagacac aaactctccct tcgctaaccac ggttagatgt cccattcattc	1565		
tcatgccctgt ataaaaactg ataaggggag agaatagttttaaaaattttc tagggtatca	1625		
taactctggt aggaagtcat ctgtctagac tcgagcaagc ttatgcattgc atgcggccg	1684		

<210> 2  
<211> 313  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg  
1 5 10 15  
Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr

Phe	Ile	Val	Leu	Ile	Gly	Gly	Leu	Val	Gly	Val	Ile	Ser	Ile	Leu	Phe
20					25						30				
35					40						45				
Leu	Leu	Val	Lys	Met	Asn	Thr	Arg	Ser	Val	Thr	Thr	Met	Ala	Val	Ile
50						55					60				
Asn	Leu	Val	Val	Val	His	Ser	Val	Phe	Leu	Leu	Thr	Val	Pro	Phe	Arg
65						70					75			80	
Leu	Thr	Tyr	Leu	Ile	Lys	Lys	Thr	Trp	Met	Phe	Gly	Leu	Pro	Phe	Cys
85						90					95				
Lys	Phe	Val	Ser	Ala	Met	Leu	His	Ile	His	Met	Tyr	Leu	Thr	Phe	Leu
100						105					110				
Phe	Tyr	Val	Val	Ile	Leu	Val	Thr	Arg	Tyr	Leu	Ile	Phe	Phe	Lys	Cys
115						120					125				
Lys	Asp	Lys	Val	Glu	Phe	Tyr	Arg	Lys	Leu	His	Ala	Val	Ala	Ala	Ser
130						135					140				
Ala	Gly	Met	Trp	Thr	Leu	Val	Ile	Val	Ile	Val	Val	Pro	Leu	Val	Val
145						150					155			160	
Ser	Arg	Tyr	Gly	Ile	His	Glu	Glu	Tyr	Asn	Glu	Glu	His	Cys	Phe	Lys
165						170					175				
Phe	His	Lys	Glu	Leu	Ala	Tyr	Thr	Val	Lys	Ile	Ile	Asn	Tyr	Met	
180						185					190				
Ile	Val	Ile	Phe	Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Leu	Val	Phe	Gln
195						200					205				
Val	Phe	Ile	Ile	Met	Leu	Met	Val	Gln	Lys	Leu	Arg	His	Ser	Leu	Leu
210						215					220				
Ser	His	Gln	Glu	Phe	Trp	Ala	Gln	Leu	Lys	Asn	Leu	Phe	Phe	Ile	Gly
225						230					235			240	
Val	Ile	Leu	Val	Cys	Phe	Leu	Pro	Tyr	Gln	Phe	Phe	Arg	Ile	Tyr	Tyr
245						250					255				
Leu	Asn	Val	Val	Thr	His	Ser	Asn	Ala	Cys	Ser	Ser	Lys	Val	Ala	Phe
260						265					270				
Tyr	Asn	Glu	Ile	Phe	Leu	Ser	Val	Thr	Ala	Ile	Ser	Cys	Tyr	Asp	Leu
275						280					285				
Leu	Leu	Phe	Val	Phe	Gly	Gly	Ser	His	Trp	Phe	Lys	Gln	Lys	Ile	Ile
290						295					300				
Gly	Leu	Trp	Asn	Cys	Val	Leu	Cys	Arg							
305						310									

<210> 3  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(939)

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Met	Gln	Lys	Cys	Asp	Phe	Pro	Ser	Met	Pro	Gly	His	Asn	Thr	Ser	Arg
1					5				10					15	
aat	tcc	tct	tgc	gat	cct	ata	gtg	aca	ccc	cac	tta	atc	agc	ctc	tac
Asn	Ser	Ser	Cys	Asp	Pro	Ile	Val	Thr	Pro	His	Leu	Ile	Ser	Leu	Tyr
20					25						30				
ttc	ata	gtg	ctt	att	ggc	ggg	ctg	gtg	ggt	gtc	att	tcc	att	ctt	ttc
Phe	Ile	Val	Ile	Gly	Gly	Leu	Val	Gly	Val	Ile	Ser	Ile	Leu	Phe	
35						40					45				
ctc	ctg	gtg	aaa	atg	aac	acc	cgg	tca	gtg	acc	acc	atg	gcg	gtc	att
Leu	Leu	Val	Lys	Met	Asn	Thr	Arg	Ser	Val	Thr	Thr	Met	Ala	Val	Ile
50						55					60				
aac	ttg	gtg	gtg	gtc	cac	agg	gtt	ttt	ctg	ctg	aca	gtg	cca	ttt	cgc
Asn	Leu	Val	Val	Val	His	Ser	Val	Phe	Leu	Leu	Thr	Val	Pro	Phe	Arg
65						70					75			80	
ttg	acc	tac	ctc	atc	aag	aag	act	tgg	atg	ttt	ggg	ctg	ccc	ttc	tgc
															288

Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys			
85	90	95	
aaa ttt gtg agt gcc atg ctg cac atc cac atg tac ctc acg ttc cta	336		
Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu			
100	105	110	
ttc tat gtg gtg atc ctg gtc acc aga tac ctc atc ttc ttc aag tgc	384		
Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys			
115	120	125	
aaa gac aaa gtg gaa ttc tac aga aaa ctg cat gct gtg gct gcc agt	432		
Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser			
130	135	140	
gct ggc atg tgg acg ctg gtg att gtc att gtg gta ccc ctg gtt gtc	480		
Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val			
145	150	155	160
tcc cgg tat gga atc cat gag gaa tac aat gag gag cac tgt ttt aaa	528		
Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys			
165	170	175	
ttt cac aaa gag ctt gct tac aca tat gtg aaa atc atc aac tat atg	576		
Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met			
180	185	190	
ata gtc att ttt gtc ata gcc gtt gct gtg att ctg ttg gtc ttc cag	624		
Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln			
195	200	205	
gtc ttc atc att atg ttg atg gtg cag aag cta cgc cac tct tta cta	672		
Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu			
210	215	220	
tcc cac cag gag ttc tgg gct cag ctg aaa aac cta ttt ttt ata ggg	720		
Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly			
225	230	235	240
gtc atc ctt gtt tgt ttc ctt ccc tac cag ttc ttt agg atc tat tac	768		
Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr			
245	250	255	
ttg aat gtt gtg acg cat tcc aat gcc tgt agc agc aag gtt gca ttt	816		
Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe			
260	265	270	
tat aac gaa atc ttc ttg agt gta aca gca att agc tgc tat gat ttg	864		
Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu			
275	280	285	
ctt ctc ttt gtc ttt ggg gga agc cat tgg ttt aag caa aag ata att	912		
Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile			
290	295	300	
ggc tta tgg aat tgt gtt ttg tgc cgt	939		
Gly Leu Trp Asn Cys Val Leu Cys Arg			
305	310		
<210> 4			
<211> 356			
<212> PRT			
<213> Mus musculus			
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Met Glu Ile Pro Ala Val Thr Glu Pro Ser Tyr Asn Thr Val Ala Lys			
1	5	10	15
Asn Asp Phe Met Ser Gly Phe Leu Cys Phe Ser Ile Asn Val Arg Ala			
20	25	30	

Phe Gly Ile Thr Val Pro Thr Pro Leu Tyr Ser Leu Val Phe Ile Ile  
     35                40                45  
 Gly Val Ile Gly His Val Leu Val Val Leu Val Leu Ile Gln His Lys  
     50                55                60  
 Arg Leu Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser  
     65                70                75                80  
 Asp Leu Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met  
     85                90                95  
 Lys Gly Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly  
     100               105               110  
 Phe Tyr Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu  
     115               120               125  
 Thr Ile Asp Arg Tyr Leu Ala Val Val His Val Val Phe Ala Leu Arg  
     130               135               140  
 Ala Arg Thr Val Thr Phe Gly Ile Ile Ser Ser Ile Ile Thr Trp Val  
     145               150               155               160  
 Leu Ala Ala Leu Val Ser Ile Pro Cys Leu Tyr Val Phe Lys Ser Gln  
     165               170               175  
 Met Glu Phe Thr Tyr His Thr Cys Arg Ala Ile Leu Pro Arg Lys Ser  
     180               185               190  
 Leu Ile Arg Phe Leu Arg Phe Gln Ala Leu Thr Met Asn Ile Leu Gly  
     195               200               205  
 Leu Ile Leu Pro Leu Leu Ala Met Ile Ile Cys Tyr Thr Arg Ile Ile  
     210               215               220  
 Asn Val Leu His Arg Arg Pro Asn Lys Lys Lys Ala Lys Val Met Arg  
     225               230               235               240  
 Leu Ile Phe Val Ile Thr Leu Leu Phe Phe Leu Leu Leu Ala Pro Tyr  
     245               250               255  
 Tyr Leu Ala Ala Phe Val Ser Ala Phe Glu Asp Val Leu Phe Thr Pro  
     260               265               270  
 Ser Cys Leu Arg Ser Gln Gln Val Asp Leu Ser Leu Met Ile Thr Glu  
     275               280               285  
 Ala Leu Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Val Phe  
     290               295               300  
 Val Gly Lys Arg Phe Arg Lys Tyr Leu Trp Gln Leu Phe Arg Arg His  
     305               310               315               320  
 Thr Ala Ile Thr Leu Pro Gln Trp Leu Pro Phe Leu Ser Glu Asp Arg  
     325               330               335  
 Ala Gln Arg Ala Ser Ala Arg Leu Pro Ser Thr Val Glu Ile Glu Thr  
     340               345               350  
 Ser Ala Asp Leu  
     355

<210> 5  
 <211> 68  
 <212> PRT  
 <213> Mus musculus

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 Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser Asp Leu  
     1                5                10                15  
 Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met Lys Gly  
     20               25               30  
 Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly Phe Tyr  
     35               40               45  
 Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu Thr Ile  
     50               55               60  
 Asp Arg Tyr Leu  
     65

<210> 6  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus

<221> VARIANT

<222> (1)...(1)  
<223> Xaa at position 1 can be G or S or T or A or  
L or I or V or M or F or Y or W or C

<221> VARIANT  
<222> (2)...(2)  
<223> Xaa at position 2 can be G or S or T or A or  
N or P or D or E

<221> VARIANT  
<222> (3)...(3)  
<223> Xaa at position 3 can not be E or D or  
P or K or R or H

<221> VARIANT  
<222> (4)...(4)  
<223> Xaa at position 4 can  
be any amino acid

<221> VARIANT  
<222> (5)...(5)  
<223> Xaa at position 5 can  
be any amino acid

<221> VARIANT  
<222> (6)...(6)  
<223> Xaa at position 6 can be L or I or V or M or  
N or Q or G or A

<221> VARIANT  
<222> (7)...(7)  
<223> Xaa at position 7 can  
be any amino acid

<221> VARIANT  
<222> (8)...(8)  
<223> Xaa at position 8 can  
be any amino acid

<221> VARIANT  
<222> (9)...(9)  
<223> Xaa at position 9 can be L or I or V or M or  
F or T

<221> VARIANT  
<222> (10)...(10)  
<223> Xaa at position 10 can be G or S or T or A or  
N or C

<221> VARIANT  
<222> (11)...(11)  
<223> Xaa at position 11 can be L or I or V or M  
or F or Y or W or S or T or A or C

<221> VARIANT  
<222> (12)...(12)  
<223> Xaa at position 12 can be D or E or N or H

<221> VARIANT  
<222> (14)...(14)  
<223> Xaa at position 14 can be F or Y or W or C  
or S or H

<221> VARIANT  
<222> (15)...(15)  
<223> Xaa at position 15  
can be any amino acid

<221> VARIANT  
<222> (16)...(16)  
<223> Xaa at position 16  
can be any amino acid

<221> VARIANT  
<222> (17)...(17)  
<223> Xaa at position 17 can be L or I or V or M

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Xaa Arg Xaa Xaa Xaa  
1 5 10 15  
Xaa